Amendments to the Claims:

This listing of claims will replace all prior versions, and listings, of claims in the application:

Listing of Claims:

Claim 1 (currently amended): A plant or yeast eukaryotic cell that comprises a prokaryotic recombinase polypeptide or a nucleic acid that encodes the prokaryotic recombinase, wherein the recombinase is capable of mediating site-specific recombination in the eukaryotic cell between an *attB* recombination site and an *attP* recombination site to form an *attL* and an *attR* site; and wherein the recombinase is not capable of mediating in the eukaryotic cell recombination between the *attL* site and the *attR* site, **wherein the recombinase is selected from the group consisting of a bacteriophage ΦC31 integrase, a coliphage P4 recombinase, a Listeria phage recombinase, a bacteriophage R4 Sre recombinase, a CisA recombinase, an XisF recombinase, and a transposon Tn*4451* TnpX recombinase.**

Claim 2 (canceled).

Claim 3 (original): The eukaryotic cell of claim 1, wherein the recombinase is a bacteriophage ΦC31 integrase.

Claim 4 (canceled).

Claim 5 (canceled).

Claim 6 (previously presented): The eukaryotic cell of claim 1, wherein the cell comprises a nucleic acid that comprises a coding sequence for the recombinase polypeptide, which coding sequence is operably linked to a promoter that mediates expression of the recombinase-encoding polynucleotide in the eukaryotic cell.

Claim 7 (original): The eukaryotic cell of claim 6, wherein the nucleic acid further comprises a selectable marker.

Claim 8 (original): The eukaryotic cell of claim 6, wherein the promoter is an inducible or a repressible promoter.

Claim 9 (previously presented): The eukaryotic cell of claim 6, wherein the nucleic acid encodes ΦC31 integrase.

Claim 10 (previously presented): The eukaryotic cell of claim 1, wherein the cell is a yeast cell.

Claim 11 (previously presented): The eukaryotic cell of claim 1, wherein the eukaryotic cell is a plant cell.

Claim 12 (previously presented): The eukaryotic cell of claim 11, wherein the eukaryotic cell is present in a plant.

Claims 13 to 35. (canceled).

Claim 36 (currently amended): A plant or yeast eukaryotic cell that comprises:

an *attP* or *attB recombination site of* bacteriophage ΦC31 integrase integrated in its genome; and

a non-genomic nucleic acid comprising a heterologous nucleic acid or a transgene, and an *attP* site if the cell has the genomic *attB* site or an *attB* site if the cell has the genomic *attP* site; **wherein the eukaryotic cell further comprises a ΦC31 integrase polypeptide**.

Claim 37 (previously presented). The eukaryotic cell of claim 36, wherein the non-genomic nucleic acid comprises the transgene.

Claims 38 to 42 (canceled).

Claim 43 (currently amended): The eukaryotic cell of claim 36, wherein the eukaryotic cell ~~further~~ comprises a nucleic acid that comprises a polynucleotide that encodes **the** **[[a]]** ΦC31 integrase polypeptide.

Claim 44 (original). The eukaryotic cell of claim 43, wherein the nucleic acid further comprises a selectable marker.

Claim 45 (currently amended): The eukaryotic cell of claim 43, wherein the nucleic acid further comprises an **inducible** promoter which **controls** ~~results in~~ expression of the ΦC31 integrase-encoding polynucleotide in the cell.

Claim 46 (canceled).

Claim 47 (previously presented): The eukaryotic cell of claim 36, wherein the plant is a dicot or a monocot.

Claim 48 (previously presented): The cell of claim 1, wherein the cell further comprises a heterologous nucleic acid or transgene located between an *attR* recombination site and an *attL* recombination site, wherein the heterologous nucleic acid or the transgene is stably integrated into the genome of the cell.

Claim 49 (previously presented): The cell of claim 48, wherein the transgene is located between the *attR* recombination site and the *attL* recombination site and is stably integrated into the genome of the cell.

Claim 50 (currently amended): The cell of claim **1** **[[2]]**, wherein the cell further comprises a heterologous nucleic acid or transgene located between an *attR* recombination site and an *attL* recombination site, wherein said heterologous nucleic acid or transgene is stably integrated into the genome of the cell.

Claim 51 (previously presented): The cell of claim 50, wherein the transgene is located between the *attR* recombination site and the *attL* recombination site and is stably integrated into the genome of the cell.

Claim 52 (currently amended): A eucaryotic somatic cell in culture **comprising**:

a prokaryotic recombinase polypeptide or a nucleic acid that encodes the prokaryotic recombinase, wherein the recombinase is capable of mediating site-specific recombination in the eukaryotic cell between an *attB* recombination site and an *attP* recombination site to form an *attL* and an *attR* site, and is not capable of mediating in the eukaryotic cell recombination between the *attL* site and the *attR* site;

~~comprising~~ **the [[an]]** *attP* or *attB* recombination site integrated in its genome;

a non-genomic nucleic acid comprising a transgene or a heterologous nucleic acid and an *attP* site if the cell has the genomic *attB* site or an *attP* site if the cell has the genomic *attB* site;

wherein the recombinase is selected from the group consisting of a bacteriophage ΦC31 integrase, a coliphage P4 recombinase, a Listeria phage recombinase, a bacteriophage R4 Sre recombinase, a CisA recombinase, an XisF recombinase, and a transposon Tn*4451* TnpX recombinase..

Claim 53 (currently amended): A non-human eukaryotic cell in culture comprising:

a prokaryotic recombinase polypeptide or a nucleic acid that encodes the prokaryotic recombinase, wherein the recombinase is capable of mediating site-specific recombination in the eukaryotic cell between an *attB* recombination site and an *attP* recombination site to form an *attL* and an *attR* site, and is not capable of mediating in the eukaryotic cell recombination between the *attL* site and the *attR* site; and

a heterologous nucleic acid or transgene located between the *attR* recombination site and the *attL* recombination site, wherein said heterologous nucleic acid or transgene is stably integrated into the genome of the cell**;**

wherein the recombinase is selected from the group consisting of a bacteriophage ΦC31 integrase, a coliphage P4 recombinase, a Listeria phage recombinase, a bacteriophage R4 Sre recombinase, a CisA recombinase, an XisF recombinase, and a transposon Tn*4451* TnpX recombinase.

Claim 54 (previously presented): The eukaryotic cell of claim 53, wherein the eukaryotic cell is selected from the group consisting of-a plant cell, a yeast cell, an insect cell and a fungal cell.

Claim 55 (previously presented): The eukaryotic cell of claim 53, wherein the eukaryotic cell is a mammalian cell.

Claim 56 (canceled).

Claim 57 (currently amended): The eukaryotic cell of claim **53** **[[56]],** wherein the recombinase is a bacteriophage ΦC31 integrase.

Claim 58 (previously presented): The eukaryotic cell of claim 53, wherein the cell is an animal cell.

Claim 59 (previously presented): The eukaryotic cell of claim 53, wherein the cell is a mouse embryonic stem cell.

Claim 60 (previously presented): The eukaryotic cell of claim 53, wherein the transgene is located between the *attR* recombination site and the *attL* recombination site and is stably integrated into the genome of the cell.

Claim 61 (currently amended): A method for obtaining site-specific recombination in a eukaryotic cell, the method comprising:

providing a eukaryotic cell that comprises an *attB* recombination site and an *attP* recombination site;

contacting the *attB* and the *attP* recombination sites with a prokaryotic recombinase polypeptide, resulting in recombination between the recombination sites, thereby forming an *attR* and an *attL* recombination site;

wherein the recombinase polypeptide can mediate site-specific recombination between the *attB* and *attP* recombination sites, but cannot mediate recombination between the *attR* and *attL* recombination sites;

wherein the recombinase is selected from the group consisting of a bacteriophage ΦC31 integrase, a coliphage P4 recombinase, a Listeria phage recombinase, a bacteriophage R4 Sre recombinase, a CisA recombinase, an XisF recombinase, and a transposon Tn*4451* TnpX recombinase.

Claim 62 (previously presented): The method of claim 61, wherein the eukaryotic cell is selected from the group consisting of a yeast cell, a fungal cell, a plant cell, an insect cell and an animal cell.

Claim 63 (previously presented): The method of claim 61, wherein the *attB* recombination site is present in a chromosome of the eukaryotic cell.

Claim 64 (previously presented): The method of claim 63, wherein the *attP* recombination site is present in a second chromosome of the eukaryotic cell and contacting the *attB* and *attP* recombination sites with the recombinase results in translocation of chromosome arms.

Claim 65 (previously presented): The method of claim 61, wherein the *attB* recombination site and the *attP* recombination site are present on a single nucleic acid molecule.

Claim 66 (previously presented): The method of claim 65, wherein the *attB* recombination site and the *attP* recombination site are in a direct orientation.

Claim 67 (previously presented): The method of claim 66, wherein the recombination results in excision of the portion of the nucleic acid molecule that lies between the *attB* and *attP* recombination sites.

Claim 68 (previously presented): The method of claim 65, wherein the *attB* recombination site and the *attP* recombination site are in an inverted orientation.

Claim 69 (previously presented): The method of claim 68, wherein the recombination results in inversion of the portion of the nucleic acid molecule that lies between the *attB* and *attP* recombination sites.

Claim 70 (previously presented): The method of claim 61, wherein the eukaryotic cell comprises a polynucleotide that encodes the recombinase polypeptide.

Claim 71 (previously presented): The method of claim 61, wherein the *attB* site is on a first linear DNA fragment and the *attP* site is on a second linear DNA fragment and contacting the *attB* and *attP* sites with the recombinase results in a translocation between the first and second linear DNA fragments.

Claim 72 (new). The eukaryotic cell of claim 52, wherein the recombinase is a bacteriophage ΦC31 integrase.